

SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT: TANZI, RUDOLPH
WASCO, WILMA

(ii) TITLE OF INVENTION: Genetic Alterations Related To Familial
Alzheimer's Disease

(iii) NUMBER OF SEQUENCES: 32

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
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(C) CITY: WASHINGTON
(D) STATE: DC
(E) COUNTRY: USA
(F) ZIP: 20005-3934

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER: To be assigned
(B) FILING DATE: Herewith
(C) CLASSIFICATION:

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: 08/706,344
(B) FILING DATE: 30-AUG-1996

(viii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: 60/003,054
(B) FILING DATE: 31-AUG-1995

(ix) ATTORNEY/AGENT INFORMATION:

(A) NAME: KIM, JUDITH U.
(B) REGISTRATION NUMBER: 40,679
(C) REFERENCE/DOCKET NUMBER: 0609.4180002

(x) TELECOMMUNICATION INFORMATION:

(A) TELEPHONE: 202-371-2600
(B) TELEFAX: 202-371-2540

(2) INFORMATION FOR SEQ ID NO: 1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 2765 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: CDS
(B) LOCATION: 249..1649

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

TGGGACAGGC AGCTCCGGGG TCCCGGGTTT CACATCGGAA ACAAAACAGC GGCTGGTCTG	60
GAAGGAAACCT GAGCTACGAG CCGCGGCGGC AGCGGGCGG CGGGGAAGCG TATACTAAT	120
CTGGGAGCCT GCAAGTGACA ACAGCCTTG CGGTCCCTAG ACAGCTTGGC CTGGAGGAGA	180
ACACATGAAA GAAAGAACCT CAAGAGGCTT TGTTTCTGT GAAACAGTAT TTCTATACAG	240
TTGCTCCA ATG ACA GAG TTA CCT GCA CCG TTG TCC TAC TTC CAG AAT GCA	290
Met Thr Glu Leu Pro Ala Pro Leu Ser Tyr Phe Gln Asn Ala	
1 5 10	
CAG ATG TCT GAG GAC AAC CAC CTG AGC AAT ACT GTA CGT AGC CAG AAT	338
Gln Met Ser Glu Asp Asn His Leu Ser Asn Thr Val Arg Ser Gln Asn	
15 20 25 30	
GAC AAT AGA GAA CGG CAG GAG CAC AAC GAC AGA CGG AGC CTT GGC CAC	386
Asp Asn Arg Glu Arg Gln Glu His Asn Asp Arg Arg Ser Leu Gly His	
35 40 45	
CCT GAG CCA TTA TCT AAT GGA CGA CCC CAG GGT AAC TCC CGG CAG GTG	434
Pro Glu Pro Leu Ser Asn Gly Arg Pro Gln Gly Asn Ser Arg Gln Val	
50 55 60	
GTG GAG CAA GAT GAG GAA GAT GAG GAG CTG ACA TTG AAA TAT GGC	482
Val Glu Gln Asp Glu Glu Asp Glu Glu Leu Thr Leu Lys Tyr Gly	
65 70 75	
GCC AAG CAT GTG ATC ATG CTC TTT GTC CCT GTG ACT CTC TGC ATG GTG	530
Ala Lys His Val Ile Met Leu Phe Val Pro Val Thr Leu Cys Met Val	
80 85 90	
GTG GTC GTG GCT ACC ATT AAG TCA GTC AGC TTT TAT ACC CGG AAG GAT	578
Val Val Val Ala Thr Ile Lys Ser Val Ser Phe Tyr Thr Arg Lys Asp	
95 100 105 110	
GGG CAG CTA ATC TAT ACC CCA TTC ACA GAA GAT ACC GAG ACT GTG GGC	626
Gly Gln Leu Ile Tyr Thr Pro Phe Thr Glu Asp Thr Glu Thr Val Gly	
115 120 125	
CAG AGA GCC CTG CAC TCA ATT CTG AAT GCT GCC ATC ATG ATC AGT GTC	674
Gln Arg Ala Leu His Ser Ile Leu Asn Ala Ala Ile Met Ile Ser Val	
130 135 140	
ATT GTT GTC ATG ACT ATC CTC CTG GTG GTT CTG TAT AAA TAC AGG TGC	722
Ile Val Val Met Thr Ile Leu Val Val Leu Tyr Lys Tyr Arg Cys	
145 150 155	
TAT AAG GTC ATC CAT GCC TGG CTT ATT ATA TCA TCT CTA TTG TTG CTG	770
Tyr Lys Val Ile His Ala Trp Leu Ile Ser Ser Leu Leu Leu Leu	
160 165 170	
TTC TTT TTT TCA TTC ATT TAC TTG GGG GAA GTG TTT AAA ACC TAT AAC	818
Phe Phe Phe Ser Phe Ile Tyr Leu Gly Glu Val Phe Lys Thr Tyr Asn	
175 180 185 190	
GTT GCT GTG GAC TAC ATT ACT GTT GCA CTC CTG ATC TGG AAT TTT GGT	866
Val Ala Val Asp Tyr Ile Thr Val Ala Leu Leu Ile Trp Asn Phe Gly	
195 200 205	

GTG GTG GGA ATG ATT TCC ATT CAC TGG AAA GGT CCA CTT CGA CTC CAG Val Val Gly Met Ile Ser Ile His Trp Lys Gly Pro Leu Arg Leu Gln 210 215 220	914
CAG GCA TAT CTC ATT ATG ATT AGT GCC CTC ATG GCC CTG GTG TTT ATC Gln Ala Tyr Leu Ile Met Ile Ser Ala Leu Met Ala Leu Val Phe Ile 225 230 235	962
AAG TAC CTC CCT GAA TGG ACT GCG TGG CTC ATC TTG GCT GTG ATT TCA Lys Tyr Leu Pro Glu Trp Thr Ala Trp Leu Ile Leu Ala Val Ile Ser 240 245 250	1010
GTA TAT GAT TTA GTG GCT GTT TTG TGT CCG AAA GGT CCA CTT CGT ATG Val Tyr Asp Leu Val Ala Val Leu Cys Pro Lys Gly Pro Leu Arg Met 255 260 265 270	1058
CTG GTT GAA ACA GCT CAG GAG AGA AAT GAA ACG CTT TTT CCA GCT CTC Leu Val Glu Thr Ala Gln Glu Arg Asn Glu Thr Leu Phe Pro Ala Leu 275 280 285	1106
ATT TAC TCC TCA ACA ATG GTG TGG TTG GTG AAT ATG GCA GAA GGA GAC Ile Tyr Ser Ser Thr Met Val Trp Leu Val Asn Met Ala Glu Gly Asp 290 295 300	1154
CCG GAA GCT CAA AGG AGA GTA TCC AAA AAT TCC AAG CAT AAT GCA GAA Pro Glu Ala Gln Arg Arg Val Ser Lys Asn Ser Lys His Asn Ala Glu 305 310 315	1202
AGC ACA GAA AGG GAG TCA CAA GAC ACT GTT GCA GAG AAT GAT GAT GGC Ser Thr Glu Arg Glu Ser Gln Asp Thr Val Ala Glu Asn Asp Asp Gly 320 325 330	1250
GGG TTC AGT GAG GAA TGG GAA GCC CAG AGG GAC AGT CAT CTA GGG CCT Gly Phe Ser Glu Glu Trp Glu Ala Gln Arg Asp Ser His Leu Gly Pro 335 340 345 350	1298
CAT CGC TCT ACA CCT GAG TCA CGA GCT GTC CAG GAA CTT TCC AGC His Arg Ser Thr Pro Glu Ser Arg Ala Ala Val Gln Glu Leu Ser Ser 355 360 365	1346
AGT ATC CTC GCT GGT GAA GAC CCA GAG GAA AGG GGA GTA AAA CTT GGA Ser Ile Leu Ala Gly Glu Asp Pro Glu Glu Arg Gly Val Lys Leu Gly 370 375 380	1394
TTG GGA GAT TTC ATT TTC TAC AGT GTT CTG GTT GGT AAA GCC TCA GCA Leu Gly Asp Phe Ile Phe Tyr Ser Val Leu Val Gly Lys Ala Ser Ala 385 390 395	1442
ACA GCC AGT GGA GAC TGG AAC ACA ACC ATA GCC TGT TTC GTA GCC ATA Thr Ala Ser Gly Asp Trp Asn Thr Thr Ile Ala Cys Phe Val Ala Ile 400 405 410	1490
TTA ATT GGT TTG TGC CTT ACA TTA TTA CTC CTT GCC ATT TTC AAG AAA Leu Ile Gly Leu Cys Leu Thr Leu Leu Leu Ala Ile Phe Lys Lys 415 420 425 430	1538
GCA TTG CCA GCT CTT CCA ATC TCC ATC ACC TTT GGG CTT GTT TTC TAC Ala Leu Pro Ala Leu Pro Ile Ser Ile Thr Phe Gly Leu Val Phe Tyr 435 440 445	1586
TTT GCC ACA GAT TAT CTT GTA CAG CCT TTT ATG GAC CAA TTA GCA TTC Phe Ala Thr Asp Tyr Leu Val Gln Pro Phe Met Asp Gln Leu Ala Phe	1634

450	455	460	
CAT CAA TTT TAT ATC TAGCATATTG GCGGGTAGAA TCCCATGGAT GTTCTTC			1689
His Gln Phe Tyr Ile			
465			
TGACTATAAC CAAATCTGGG GAGGACAAAG GTGATTTCC TGTGTCCACA TCTAACAAAG			1749
TCAAGATTCC CGGCTGGACT TTTGCAGCTT CCTTCCAAGT CTTCTGACC ACCTTGCAC			1809
ATTGGACTTT GGAAGGAGGT GCCTATAGAA AACGATTTG AACATACTTC ATCGCAGTGG			1869
ACTGTGTCCC TCGGTGCAGA AACTACCAGA TTTGAGGGAC GAGGTCAAGG AGATATGATA			1929
GGCCCGGAAG TTGCTGTGCC CCATCAGCAG CTTGACGCGT GGTCACAGGA CGATTTCACT			1989
GACACTGCGA ACTCTCAGGA CTACCGTTA CCAAGAGGTT AGGTGAAGTG GTTAAACCA			2049
AACGGAACTC TTCATCTTAA ACTACACGTT GAAAATCAAC CCAATAATTC TGTATTAAC			2109
GAATTCTGAA CTTTCAGGA GGTACTGTGA GGAAGAGCAG GCACCAGCAG CAGAATGGGG			2169
AATGGAGAGG TGGGCAGGGG TTCCAGCTTC CCTTGATTT TTTGCTGCAG ACTCATCCTT			2229
TTTAAATGAG ACTTGTTC CCCTCTCTT GAGTCAAGTC AAATATGTAG ATTGCCTTG			2289
GCAATTCTTC TTCTCAAGCA CTGACACTCA TTACCGTCTG TGATTGCCAT TTCTTCCCAA			2349
GGCCAGTCTG AACCTGAGGT TGCTTATCC TAAAAGTTT AACCTCAGGT TCCAAATTCA			2409
GTAAATTTG GAAACAGTAC AGCTATTTCT CATCAATTCT CTATCATGTT GAAGTCAAAT			2469
TTGGATTTTC CACCAAATTC TGAATTGTA GACATACTTG TACGCTCACT TGCCCCAGA			2529
TGCCTCCTCT GTCCTCATTC TTCTCTCCCA CACAAGCAGT CTTTTCTAC AGCCAGTAAG			2589
GCAGCTCTGT CRTGGTAGCA GATGGTCCCA TTATTCTAGG GTCTTACTCT TTGTATGATG			2649
AAAAGAATGT GTTATGAATC GGTGCTGTCA GCCCTGCTGT CAGACCTTCT TCCACAGCAA			2709
ATGAGATGTA TGCCCAAAGC GGTAGAATTA AAGAAGAGTA AAATGGCTGT TGAAGC			2765

(2) INFORMATION FOR SEQ ID NO: 2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 467 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

Met	Thr	Glu	Leu	Pro	Ala	Pro	Leu	Ser	Tyr	Phe	Gln	Asn	Ala	Gln	Met
1							5			10				15	

Ser	Glu	Asp	Asn	His	Leu	Ser	Asn	Thr	Val	Arg	Ser	Gln	Asn	Asp	Asn
					20			25					30		

Arg	Glu	Arg	Gln	Glu	His	Asn	Asp	Arg	Arg	Ser	Leu	Gly	His	Pro	Glu
						35		40				45			

Pro Leu Ser Asn Gly Arg Pro Gln Gly Asn Ser Arg Gln Val Val Glu
50 55 60

Gln Asp Glu Glu Glu Asp Glu Glu Leu Thr Leu Lys Tyr Gly Ala Lys
65 70 75 80

His Val Ile Met Leu Phe Val Pro Val Thr Leu Cys Met Val Val Val
85 90 95

Val Ala Thr Ile Lys Ser Val Ser Phe Tyr Thr Arg Lys Asp Gly Gln
100 105 110

Leu Ile Tyr Thr Pro Phe Thr Glu Asp Thr Glu Thr Val Gly Gln Arg
115 120 125

Ala Leu His Ser Ile Leu Asn Ala Ala Ile Met Ile Ser Val Ile Val
130 135 140

Val Met Thr Ile Leu Leu Val Val Leu Tyr Lys Tyr Arg Cys Tyr Lys
145 150 155 160

Val Ile His Ala Trp Leu Ile Ile Ser Ser Leu Leu Leu Leu Phe Phe
165 170 175

Phe Ser Phe Ile Tyr Leu Gly Glu Val Phe Lys Thr Tyr Asn Val Ala
180 185 190

Val Asp Tyr Ile Thr Val Ala Leu Leu Ile Trp Asn Phe Gly Val Val
195 200 205

Gly Met Ile Ser Ile His Trp Lys Gly Pro Leu Arg Leu Gln Gln Ala
210 215 220

Tyr Leu Ile Met Ile Ser Ala Leu Met Ala Leu Val Phe Ile Lys Tyr
225 230 235 240

Leu Pro Glu Trp Thr Ala Trp Leu Ile Leu Ala Val Ile Ser Val Tyr
245 250 255

Asp Leu Val Ala Val Leu Cys Pro Lys Gly Pro Leu Arg Met Leu Val
260 265 270

Glu Thr Ala Gln Glu Arg Asn Glu Thr Leu Phe Pro Ala Leu Ile Tyr
275 280 285

Ser Ser Thr Met Val Trp Leu Val Asn Met Ala Glu Gly Asp Pro Glu
290 295 300

Ala Gln Arg Arg Val Ser Lys Asn Ser Lys His Asn Ala Glu Ser Thr
305 310 315 320

Glu Arg Glu Ser Gln Asp Thr Val Ala Glu Asn Asp Asp Gly Gly Phe
325 330 335

Ser Glu Glu Trp Glu Ala Gln Arg Asp Ser His Leu Gly Pro His Arg
340 345 350

Ser Thr Pro Glu Ser Arg Ala Ala Val Gln Glu Leu Ser Ser Ser Ile
355 360 365

Leu Ala Gly Glu Asp Pro Glu Glu Arg Gly Val Lys Leu Gly Leu Gly
370 375 380

Asp Phe Ile Phe Tyr Ser Val Leu Val Gly Lys Ala Ser Ala Thr Ala
385 390 395 400

Ser Gly Asp Trp Asn Thr Thr Ile Ala Cys Phe Val Ala Ile Leu Ile
405 410 415

Gly Leu Cys Leu Thr Leu Leu Leu Ala Ile Phe Lys Lys Ala Leu
420 425 430

Pro Ala Leu Pro Ile Ser Ile Thr Phe Gly Leu Val Phe Tyr Phe Ala
435 440 445

Thr Asp Tyr Leu Val Gln Pro Phe Met Asp Gln Leu Ala Phe His Gln
450 455 460

Phe Tyr Ile
465

(2) INFORMATION FOR SEQ ID NO: 3:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 2765 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (ix) FEATURE:
- (A) NAME/KEY: CDS
 - (B) LOCATION: 249..1649

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

TGGGACAGGC AGCTCCGGGG TCCGCGGTTT CACATCGGAA ACAAAACAGC GGCTGGTCTG 60
GAAGGAACCT GAGCTACGAG CCGCGGCCGC AGCGGGCGG CGGGGAAGCG TATACTAAT 120
CTGGGAGCCT GCAAGTGACA ACAGCCTTG CGGTCCCTAG ACAGCTTGGC CTGGAGGAGA 180
ACACATGAAA GAAAGAACCT CAAGAGGCTT TGTTTCTGT GAAACAGTAT TTCTATACAG 240
TTGCTCCA ATG ACA GAG TTA CCT GCA CCG TTG TCC TAC TTC CAG AAT GCA 290
Met Thr Glu Leu Pro Ala Pro Leu Ser Tyr Phe Gln Asn Ala
1 5 10

CAG ATG TCT GAG GAC AAC CAC CTG AGC AAT ACT GTA CGT AGC CAG AAT 338
Gln Met Ser Glu Asp Asn His Leu Ser Asn Thr Val Arg Ser Gln Asn
15 20 25 30

GAC AAT AGA GAA CGG CAG GAG CAC AAC GAC AGA CGG AGC CTT GGC CAC 386
Asp Asn Arg Glu Arg Gln Glu His Asn Asp Arg Arg Ser Leu Gly His
35 40 45

CCT GAG CCA TTA TCT AAT GGA CGA CCC CAG GGT AAC TCC CGG CAG GTG 434
Pro Glu Pro Leu Ser Asn Gly Arg Pro Gln Gly Asn Ser Arg Gln Val
50 55 60

GTG GAG CAA GAT GAG GAA GAT GAG GAG CTG ACA TTG AAA TAT GGC 482
Val Glu Gln Asp Glu Glu Asp Glu Glu Leu Thr Leu Lys Tyr Gly

65	70	75	
GCC AAG CAT GTG ATC ATG CTC TTT GTC CCT GTG ACT CTC TGC ATG GTG Ala Lys His Val Ile Met Leu Phe Val Pro Val Thr Leu Cys Met Val 80 85 90			530
GTG GTC GTG GCT ACC ATT AAG TCA GTC AGC TTT TAT ACC CGG AAG GAT Val Val Val Ala Thr Ile Lys Ser Val Ser Phe Tyr Thr Arg Lys Asp 95 100 105 110			578
GGG CAG CTA ATC TAT ACC CCA TTC ACA GAA GAT ACC GAG ACT GTG GGC Gly Gln Leu Ile Tyr Thr Pro Phe Thr Glu Asp Thr Glu Thr Val Gly 115 120 125			626
CAG AGA GCC CTG CAC TCA ATT CTG AAT GCT GCC ATC ATG ATC AGT GTC Gln Arg Ala Leu His Ser Ile Leu Asn Ala Ala Ile Met Ile Ser Val 130 135 140			674
ATT GTT GTC ATG ACT ATC CTC CTG GTG GTT CTG TAT AAA TAC AGG TGC Ile Val Val Met Thr Ile Leu Leu Val Val Leu Tyr Lys Tyr Arg Cys 145 150 155			722
TAT AAG GTC ATC CAT GCC TGG CTT ATT ATA TCA TCT CTA TTG TTG CTG Tyr Lys Val Ile His Ala Trp Leu Ile Ser Ser Leu Leu Leu Leu 160 165 170			770
TTC TTT TTT TCA TTC ATT TAC TTG GGG GAA GTG TTT AAA ACC TAT AAC Phe Phe Phe Ser Phe Ile Tyr Leu Gly Glu Val Phe Lys Thr Tyr Asn 175 180 185 190			818
GTT GCT GTG GAC TAC ATT ACT GTT GCA CTC CTG ATC TGG AAT TTT GGT Val Ala Val Asp Tyr Ile Thr Val Ala Leu Leu Ile Trp Asn Phe Gly 195 200 205			866
GTG GTG GGA ATG ATT TCC ATT CAC TGG AAA GGT CCA CTT CGA CTC CAG Val Val Gly Met Ile Ser Ile His Trp Lys Gly Pro Leu Arg Leu Gln 210 215 220			914
CAG GCA TAT CTC ATT ATG ATT AGT GCC CTC ATG GCC CTG GTG TTT ATC Gln Ala Tyr Leu Ile Met Ile Ser Ala Leu Met Ala Leu Val Phe Ile 225 230 235			962
AAG TAC CTC CCT GAA TGG ACT GCG TGG CTC ATC TTG GCT GTG ATT TCA Lys Tyr Leu Pro Glu Trp Thr Ala Trp Leu Ile Leu Ala Val Ile Ser 240 245 250			1010
GTA TAT GAT TTA GTG GCT GTT TTG CGT CTG AAA GGT CCA CTT CAT ATG Val Tyr Asp Leu Val Ala Val Leu Arg Leu Lys Gly Pro Leu His Met 255 260 265 270			1058
CTG GTT GAA ACA GCT CAG GAG AGA AAT GAA ACG CTT TTT CCA GCT CTC Leu Val Glu Thr Ala Gln Glu Arg Asn Glu Thr Leu Phe Pro Ala Leu 275 280 285			1106
ATT TAC TCC TCA ACA ATG GTG TGG TTG GTG AAT ATG GCA GAA GGA GAC Ile Tyr Ser Ser Thr Met Val Trp Leu Val Asn Met Ala Glu Gly Asp 290 295 300			1154
CCG GAA GCT CAA AGG AGA GTA TCC AAA AAT TCC AAG CAT AAT GCA GAA Pro Glu Ala Gln Arg Arg Val Ser Lys Asn Ser Lys His Asn Ala Glu 305 310 315			1202

AGC ACA GAA AGG GAG TCA CAA GAC ACT GTT GCA GAG AAT GAT GAT GGC Ser Thr Glu Arg Glu Ser Gln Asp Thr Val Ala Glu Asn Asp Asp Gly 320 325 330	1250
GGG TTC AGT GAG GAA TGG GAA GCC CAG AGG GAC AGT CAT CTA GGG CCT Gly Phe Ser Glu Glu Trp Glu Ala Gln Arg Asp Ser His Leu Gly Pro 335 340 345 350	1298
CAT CGC TCT ACA CCT GAG TCA CGA GCT GCT GTC CAG GAA CTT TCC AGC His Arg Ser Thr Pro Glu Ser Arg Ala Ala Val Gln Glu Leu Ser Ser 355 360 365	1346
AGT ATC CTC GCT GGT GAA GAC CCA GAG GAA AGG GGA GTA AAA CTT GGA Ser Ile Leu Ala Gly Glu Asp Pro Glu Glu Arg Gly Val Lys Leu Gly 370 375 380	1394
TTG GGA GAT TTC ATT TTC TAC AGT GTT CTG GTT GGT AAA GCC TCA GCA Leu Gly Asp Phe Ile Phe Tyr Ser Val Leu Val Gly Lys Ala Ser Ala 385 390 395	1442
ACA GCC AGT GGA GAC TGG AAC ACA ACC ATA GCC TGT TTC GTA GCC ATA Thr Ala Ser Gly Asp Trp Asn Thr Thr Ile Ala Cys Phe Val Ala Ile 400 405 410	1490
TTA ATT GGT TTG TGC CTT ACA TTA TTA CTC CTT GCC ATT TTC AAG AAA Leu Ile Gly Leu Cys Leu Thr Leu Leu Leu Ala Ile Phe Lys Lys 415 420 425 430	1538
GCA TTG CCA GCT CTT CCA ATC TCC ATC ACC TTT GGG CTT GTT TTC TAC Ala Leu Pro Ala Leu Pro Ile Ser Ile Thr Phe Gly Leu Val Phe Tyr 435 440 445	1586
TTT GCC ACA GAT TAT CTT GTA CAG CCT TTT ATG GAC CAA TTA GCA TTC Phe Ala Thr Asp Tyr Leu Val Gln Pro Phe Met Asp Gln Leu Ala Phe 450 455 460	1634
CAT CAA TTT TAT ATC TAGCATATTG GCGGTTAGAA TCCCATGGAT GTTTCTTCTT His Gln Phe Tyr Ile 465	1689
TGACTATAAC CAAATCTGGG GAGGACAAAG GTGATTTCC TGTGTCCACA TCTAACAAAG	1749
TCAAGATTCC CGGCTGGACT TTTGCAGCTT CCTTCCAAGT CTTCCTGACC ACCTTGCAC	1809
ATTGGACTTT GGAAGGAGGT GCCTATAGAA AACGATTTG AACATACTTC ATCGCAGTGG	1869
ACTGTGTCCC TCGGTGCAGA AACTACCAGA TTTGAGGGAC GAGGTCAAGG AGATATGATA	1929
GGCCCGGAAG TTGCTGTGCC CCATCAGCAG CTTGACGCGT GGTCACAGGA CGATTCACT	1989
GACACTGCGA ACTCTCAGGA CTACCGGTTA CCAAGAGGTT AGGTGAAGTG GTTAAACCA	2049
AACGGAACTC TTCATCTTAA ACTACACGTT GAAAATCAAC CCAATAATTC TGTATTAAC	2109
GAATTCTGAA CTTTCAGGA GGTACTGTGA GGAAGAGCAG GCACCAGCAG CAGAATGGGG	2169
AATGGAGAGG TGGGCAGGGG TTCCAGCTTC CCTTGATTT TTTGCTGCAG ACTCATCCTT	2229
TTTAAATGAG ACTTGTGTTTC CCCTCTCTTT GAGTCAAGTC AAATATGTAG ATTGCCTTG	2289
GCAATTCTTC TTCTCAAGCA CTGACACTCA TTACCGTCTG TGATTGCCAT TTCTTCCCAA	2349

GGCCAGTCTG AACCTGAGGT TGCTTTATCC TAAAAGTTT AACCTCAGGT TCCAAATTCA	2409
GTAAATTTG GAAACAGTAC AGCTATTCT CATCAATTCT CTATCATGTT GAAGTCAAAT	2469
TTGGATTTTC CACCAAATTC TGAATTGTA GACATACTTG TACGCTCACT TGCCCCCAGA	2529
TGCCTCCTCT GTCCTCATTC TTCTCTCCA CACAAGCAGT CTTTTCTAC AGCCAGTAAG	2589
GCAGCTCTGT CRTGGTAGCA GATGGTCCC TTATTCTAGG GTCTTACTCT TTGTATGATG	2649
AAAAGAATGT GTTATGAATC GGTGCTGTCA GCCCTGCTGT CAGACCTTCT TCCACAGCAA	2709
ATGAGATGTA TGCCAAAGC GGTAGAATTA AAGAAGAGTA AAATGGCTGT TGAAGC	2765

(2) INFORMATION FOR SEQ ID NO: 4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 467 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:

Met Thr Glu Leu Pro Ala Pro Leu Ser Tyr Phe Gln Asn Ala Gln Met	
1 5 10 15	
Ser Glu Asp Asn His Leu Ser Asn Thr Val Arg Ser Gln Asn Asp Asn	
20 25 30	
Arg Glu Arg Gln Glu His Asn Asp Arg Arg Ser Leu Gly His Pro Glu	
35 40 45	
Pro Leu Ser Asn Gly Arg Pro Gln Gly Asn Ser Arg Gln Val Val Glu	
50 55 60	
Gln Asp Glu Glu Glu Asp Glu Glu Leu Thr Leu Lys Tyr Gly Ala Lys	
65 70 75 80	
His Val Ile Met Leu Phe Val Pro Val Thr Leu Cys Met Val Val Val	
85 90 95	
Val Ala Thr Ile Lys Ser Val Ser Phe Tyr Thr Arg Lys Asp Gly Gln	
100 105 110	
Leu Ile Tyr Thr Pro Phe Thr Glu Asp Thr Glu Thr Val Gly Gln Arg	
115 120 125	
Ala Leu His Ser Ile Leu Asn Ala Ala Ile Met Ile Ser Val Ile Val	
130 135 140	
Val Met Thr Ile Leu Leu Val Val Leu Tyr Lys Tyr Arg Cys Tyr Lys	
145 150 155 160	
Val Ile His Ala Trp Leu Ile Ile Ser Ser Leu Leu Leu Leu Phe Phe	
165 170 175	
Phe Ser Phe Ile Tyr Leu Gly Glu Val Phe Lys Thr Tyr Asn Val Ala	
180 185 190	
Val Asp Tyr Ile Thr Val Ala Leu Leu Ile Trp Asn Phe Gly Val Val	

195	200	205
Gly Met Ile Ser Ile His Trp Lys Gly Pro Leu Arg Leu Gln Gln Ala		
210	215	220
Tyr Leu Ile Met Ile Ser Ala Leu Met Ala Leu Val Phe Ile Lys Tyr		
225	230	235
240		
Leu Pro Glu Trp Thr Ala Trp Leu Ile Leu Ala Val Ile Ser Val Tyr		
245	250	255
Asp Leu Val Ala Val Leu Arg Leu Lys Gly Pro Leu His Met Leu Val		
260	265	270
Glu Thr Ala Gln Glu Arg Asn Glu Thr Leu Phe Pro Ala Leu Ile Tyr		
275	280	285
Ser Ser Thr Met Val Trp Leu Val Asn Met Ala Glu Gly Asp Pro Glu		
290	295	300
Ala Gln Arg Arg Val Ser Lys Asn Ser Lys His Asn Ala Glu Ser Thr		
305	310	315
320		
Glu Arg Glu Ser Gln Asp Thr Val Ala Glu Asn Asp Asp Gly Gly Phe		
325	330	335
Ser Glu Glu Trp Glu Ala Gln Arg Asp Ser His Leu Gly Pro His Arg		
340	345	350
Ser Thr Pro Glu Ser Arg Ala Ala Val Gln Glu Leu Ser Ser Ser Ile		
355	360	365
Leu Ala Gly Glu Asp Pro Glu Glu Arg Gly Val Lys Leu Gly Leu Gly		
370	375	380
Asp Phe Ile Phe Tyr Ser Val Leu Val Gly Lys Ala Ser Ala Thr Ala		
385	390	395
400		
Ser Gly Asp Trp Asn Thr Thr Ile Ala Cys Phe Val Ala Ile Leu Ile		
405	410	415
Gly Leu Cys Leu Thr Leu Leu Leu Ala Ile Phe Lys Lys Ala Leu		
420	425	430
Pro Ala Leu Pro Ile Ser Ile Thr Phe Gly Leu Val Phe Tyr Phe Ala		
435	440	445
Thr Asp Tyr Leu Val Gln Pro Phe Met Asp Gln Leu Ala Phe His Gln		
450	455	460
Phe Tyr Ile		
465		

(2) INFORMATION FOR SEQ ID NO: 5:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:

CACCCATTAA CAAGTTTAGC

20

(2) INFORMATION FOR SEQ ID NO: 6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:

GATGAGACAA GTGCCGTGAA

20

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 38 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

Gly Gln Ala Ala Pro Gly Ser Ala Val Ser His Arg Lys Gln Asn Ser
1 5 10 15

Gly Trp Ser Gly Arg Asn Leu Ser Tyr Glu Pro Arg Arg Gln Arg Gly
20 25 30

Gly Gly Glu Ala Tyr Thr
35

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

Ser Gly Ser Leu Gln Val Thr Thr Ala Phe Ala Val Leu Arg Gln Leu
1 5 10 15

Gly Leu Glu Glu Asn Thr
20

(2) INFORMATION FOR SEQ ID NO:9:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

Lys Lys Glu Pro Gln Glu Ala Leu Phe Ser Val Lys Gln Tyr Phe Tyr
1 5 10 15

Thr Val Ala Pro
20

(2) INFORMATION FOR SEQ ID NO:10:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 4 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

His Ile Cys Gly
1

(2) INFORMATION FOR SEQ ID NO:11:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 60 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

Asn Pro Met Asp Val Ser Ser Leu Thr Ile Thr Lys Ser Gly Glu Asp
1 5 10 15

Lys Gly Asp Phe Pro Val Ser Thr Ser Asn Lys Val Lys Ile Pro Gly
20 25 30

Trp Thr Phe Ala Ala Ser Phe Gln Val Phe Leu Thr Thr Leu His Tyr
35 40 45

Trp Thr Leu Glu Gly Gly Ala Tyr Arg Lys Arg Phe
50 55 60

(2) INFORMATION FOR SEQ ID NO:12:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 17 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

Thr Tyr Phe Ile Ala Val Asp Cys Val Pro Arg Cys Arg Asn Tyr Gln
1 5 10 15

Ile

(2) INFORMATION FOR SEQ ID NO:13:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 19 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

Gly Thr Arg Ser Arg Arg Tyr Asp Arg Pro Gly Ser Cys Cys Ala Pro
1 5 10 15

Ser Ala Ala

(2) INFORMATION FOR SEQ ID NO:14:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 8 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

Arg Val Val Thr Gly Arg Phe His
1 5

(2) INFORMATION FOR SEQ ID NO:15:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 17 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

His Cys Glu Leu Ser Gly Leu Pro Val Thr Lys Arg Leu Gly Glu Val
1 5 10 15
Val

(2) INFORMATION FOR SEQ ID NO:16:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 7 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

Thr Lys Arg Asn Ser Ser Ser
1 5

(2) INFORMATION FOR SEQ ID NO:17:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 4 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

Lys Ser Thr Gln
1

(2) INFORMATION FOR SEQ ID NO:18:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 4 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

Phe Cys Ile Asn
1

(2) INFORMATION FOR SEQ ID NO:19:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 40 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

Ile Leu Asn Phe Ser Gly Gly Thr Val Arg Lys Ser Arg His Gln Gln
1 5 10 15

Gln Asn Gly Glu Trp Arg Gly Gln Gly Phe Gln Leu Pro Phe Asp
20 25 30

Phe Leu Leu Gln Thr His Pro Phe
35 40

(2) INFORMATION FOR SEQ ID NO:20:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 8 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

Met Arg Leu Val Phe Pro Ser Leu
1 5

(2) INFORMATION FOR SEQ ID NO:21:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 5 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

Val Lys Ser Asn Met
1 5

(2) INFORMATION FOR SEQ ID NO:22:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 26 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

Ile Ala Phe Gly Asn Ser Ser Ser Gln Ala Leu Thr Leu Ile Thr Val
1 5 10 15
Cys Asp Cys His Phe Phe Pro Arg Pro Val
20 25

(2) INFORMATION FOR SEQ ID NO:23:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 41 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

Gly Cys Phe Ile Leu Lys Val Leu Thr Ser Gly Ser Lys Phe Ser Lys
1 5 10 15
Phe Trp Lys Gln Tyr Ser Tyr Phe Ser Ser Ile Leu Tyr His Val Glu
20 25 30
Val Lys Phe Gly Phe Ser Thr Lys Phe
35 40

(2) INFORMATION FOR SEQ ID NO:24:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 31 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

Ile	Cys	Arg	His	Thr	Cys	Thr	Leu	Thr	Cys	Pro	Gln	Met	Pro	Pro	Leu
1				5					10					15	
Ser	Ser	Phe	Phe	Ser	Pro	Thr	Gln	Ala	Val	Phe	Phe	Tyr	Ser	Gln	
				20					25				30		

(2) INFORMATION FOR SEQ ID NO:25:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 25 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

Gly	Ser	Ser	Val	Xaa	Val	Ala	Asp	Gly	Pro	Ile	Ile	Leu	Gly	Ser	Tyr
1					5				10					15	
Ser	Leu	Tyr	Asp	Glu	Lys	Asn	Val	Leu							
			20					25							

(2) INFORMATION FOR SEQ ID NO:26:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 27 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

Ile	Gly	Ala	Val	Ser	Pro	Ala	Val	Arg	Pro	Ser	Ser	Thr	Ala	Asn	Glu
1				5				10						15	
Met	Tyr	Ala	Gln	Ser	Gly	Arg	Ile	Lys	Glu	Glu					
				20					25						

(2) INFORMATION FOR SEQ ID NO: 27:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 2765 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (ix) FEATURE:
(A) NAME/KEY: CDS
(B) LOCATION: 249..1649

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 27:

TGGGACAGGC AGCTCCGGGG TCCGCGGTTT CACATCGGAA ACAAAACAGC GGCTGGTCTG	60
GAAGGAAACCT GAGCTACGAG CCGCGGCCGG AGCGGGGCGG CGGGGAAGCG TATACTTAAT	120
CTGGGAGCCT GCAAGTGACA ACAGCCTTTG CGGTCTTAG ACAGCTTGGC CTGGAGGAGA	180
ACACATGAAA GAAAGAACCT CAAGAGGCTT TGTTTCTGT GAAACAGTAT TTCTATACAG	240
TTGCTCCA ATG ACA GAG TTA CCT GCA CCG TTG TCC TAC TTC CAG AAT GCA	290
Met Thr Glu Leu Pro Ala Pro Leu Ser Tyr Phe Gln Asn Ala	
1 5 10	
CAG ATG TCT GAG GAC AAC CAC CTG AGC AAT ACT GTA CGT AGC CAG AAT	338
Gln Met Ser Glu Asp Asn His Leu Ser Asn Thr Val Arg Ser Gln Asn	
15 20 25 30	
GAC AAT AGA GAA CGG CAG GAG CAC AAC GAC AGA CGG AGC CTT GGC CAC	386
Asp Asn Arg Glu Arg Gln Glu His Asn Asp Arg Arg Ser Leu Gly His	
35 40 45	
CCT GAG CCA TTA TCT AAT GGA CGA CCC CAG GGT AAC TCC CGG CAG GTG	434
Pro Glu Pro Leu Ser Asn Gly Arg Pro Gln Gly Asn Ser Arg Gln Val	
50 55 60	
GTG GAG CAA GAT GAG GAA GAT GAG GAG CTG ACA TTG AAA TAT GGC	482
Val Glu Gln Asp Glu Glu Asp Glu Glu Leu Thr Leu Lys Tyr Gly	
65 70 75	
GCC AAG CAT GTG ATC ATG CTC TTT GTC CCT GTG ACT CTC TGC ATG GTG	530
Ala Lys His Val Ile Met Leu Phe Val Pro Val Thr Leu Cys Met Val	
80 85 90	
GTG GTC GTG GCT ACC ATT AAG TCA GTC AGC TTT TAT ACC CGG AAG GAT	578
Val Val Val Ala Thr Ile Lys Ser Val Ser Phe Tyr Thr Arg Lys Asp	
95 100 105 110	
GGG CAG CTA ATC TAT ACC CCA TTC ACA GAA GAT ACC GAG ACT GTG GGC	626
Gly Gln Leu Ile Tyr Thr Pro Phe Thr Glu Asp Thr Glu Thr Val Gly	
115 120 125	
CAG AGA GCC CTG CAC TCA ATT CTG AAT GCT GCC ATC ATG ATC AGT GTC	674
Gln Arg Ala Leu His Ser Ile Leu Asn Ala Ala Ile Met Ile Ser Val	
130 135 140	
ATT GTT GTC ATG ACT ATC CTC CTG GTG GTT CTG TAT AAA TAC AGG TGC	722

Ile Val Val Met Thr Ile Leu Leu Val Val Leu Tyr Lys Tyr Arg Cys			
145	150	155	
TAT AAG GTC ATC CAT GCC TGG CTT ATT ATA TCA TCT CTA TTG TTG CTG			770
Tyr Lys Val Ile His Ala Trp Leu Ile Ser Ser Leu Leu Leu Leu			
160	165	170	
TTC TTT TTT TCA TTC ATT TAC TTG GGG GAA GTG TTT AAA ACC TAT AAC			818
Phe Phe Phe Ser Phe Ile Tyr Leu Gly Glu Val Phe Lys Thr Tyr Asn			
175	180	185	190
GTT GCT GTG GAC TAC ATT ACT GTT GCA CTC CTG ATC TGG AAT TTT GGT			866
Val Ala Val Asp Tyr Ile Thr Val Ala Leu Leu Ile Trp Asn Phe Gly			
195	200	205	
GTG GTG GGA ATG ATT TCC ATT CAC TGG AAA GGT CCA CTT CGA CTC CAG			914
Val Val Gly Met Ile Ser Ile His Trp Lys Gly Pro Leu Arg Leu Gln			
210	215	220	
CAG GCA TAT CTC ATT ATG ATT AGT GCC CTC ATG GCC CTG GTG TTT ATC			962
Gln Ala Tyr Leu Ile Met Ile Ser Ala Leu Met Ala Leu Val Phe Ile			
225	230	235	
AAG TAC CTC CCT GAA TGG ACT GCG TGG CTC ATC TTG GCT GTG ATT TCA			1010
Lys Tyr Leu Pro Glu Trp Thr Ala Trp Leu Ile Leu Ala Val Ile Ser			
240	245	250	
GTA TAT GAT TTA GTG GCT GTT TTG CGT CCG AAA GGT CCA CTT CGT ATG			1058
Val Tyr Asp Leu Val Ala Val Leu Arg Pro Lys Gly Pro Leu Arg Met			
255	260	265	270
CTG GTT GAA ACA GCT CAG GAG AGA AAT GAA ACG CTT TTT CCA GCT CTC			1106
Leu Val Glu Thr Ala Gln Glu Arg Asn Glu Thr Leu Phe Pro Ala Leu			
275	280	285	
ATT TAC TCC TCA ACA ATG GTG TGG TTG GTG AAT ATG GCA GAA GGA GAC			1154
Ile Tyr Ser Ser Thr Met Val Trp Leu Val Asn Met Ala Glu Gly Asp			
290	295	300	
CCG GAA GCT CAA AGG AGA GTA TCC AAA AAT TCC AAG CAT AAT GCA GAA			1202
Pro Glu Ala Gln Arg Arg Val Ser Lys Asn Ser Lys His Asn Ala Glu			
305	310	315	
AGC ACA GAA AGG GAG TCA CAA GAC ACT GTT GCA GAG AAT GAT GAT GGC			1250
Ser Thr Glu Arg Glu Ser Gln Asp Thr Val Ala Glu Asn Asp Asp Gly			
320	325	330	
GGG TTC AGT GAG GAA TGG GAA GCC CAG AGG GAC AGT CAT CTA GGG CCT			1298
Gly Phe Ser Glu Glu Trp Glu Ala Gln Arg Asp Ser His Leu Gly Pro			
335	340	345	350
CAT CGC TCT ACA CCT GAG TCA CGA GCT GCT GTC CAG GAA CTT TCC AGC			1346
His Arg Ser Thr Pro Glu Ser Arg Ala Ala Val Gln Glu Leu Ser Ser			
355	360	365	
AGT ATC CTC GCT GGT GAA GAC CCA GAG GAA AGG GGA GTA AAA CTT GGA			1394
Ser Ile Leu Ala Gly Glu Asp Pro Glu Glu Arg Gly Val Lys Leu Gly			
370	375	380	
TTG GGA GAT TTC ATT TTC TAC AGT GTT CTG GTT GGT AAA GCC TCA GCA			1442
Leu Gly Asp Phe Ile Phe Tyr Ser Val Leu Val Gly Lys Ala Ser Ala			
385	390	395	

ACA	GCC	AGT	GGA	GAC	TGG	AAC	ACA	ACC	ATA	GCC	TGT	TTC	GTA	GCC	ATA	1490
Thr	Ala	Ser	Gly	Asp	Trp	Asn	Thr	Thr	Ile	Ala	Cys	Phe	Val	Ala	Ile	
400							405								410	
TTA	ATT	GGT	TTG	TGC	CTT	ACA	TTA	CTA	CTC	CTT	GCC	ATT	TTC	AAG	AAA	1538
Leu	Ile	Gly	Leu	Cys	Leu	Thr	Leu	Leu	Leu	Ala	Ile	Phe	Lys	Lys		
415							420					425			430	
GCA	TTG	CCA	GCT	CTT	CCA	ATC	TCC	ATC	ACC	TTT	GGG	CTT	GTT	TTC	TAC	1586
Ala	Leu	Pro	Ala	Leu	Pro	Ile	Ser	Ile	Thr	Phe	Gly	Leu	Val	Phe	Tyr	
							435					440			445	
TTT	GCC	ACA	GAT	TAT	CTT	GTA	CAG	CCT	TTT	ATG	GAC	CAA	TTA	GCA	TTC	1634
Phe	Ala	Thr	Asp	Tyr	Leu	Val	Gln	Pro	Phe	Met	Asp	Gln	Leu	Ala	Phe	
							450					455			460	
CAT	CAA	TTT	TAT	ATC	TAGCATATT	TTT	CGGGTTAGAA	TCCCATGGAT	TCCCATGGAT	TTT	CATGGAT	TTT	CATGGAT	TTT	CATGGAT	1689
His	Gln	Phe	Tyr	Ile												
							465									
TGACTATAAC	CAAATCTGGG	GAGGACAAAG	GTGATTTCC	TGTGTCCACA	TCTAACAAAG											1749
TCAAGATTCC	CGGCTGGACT	TTTGCAGCTT	CCTTCCAAGT	CTTCCTGACC	ACCTTGCACT											1809
ATTGGACTTT	GGAAGGAGGT	GCCTATAGAA	AACGATTTG	AACATACTTC	ATCGCAGTGG											1869
ACTGTGTCCC	TCGGTGCAGA	AACTACCAGA	TTTGAGGGAC	GAGGTCAAGG	AGATATGATA											1929
GGCCCGGAAG	TTGCTGTGCC	CCATCAGCAG	CTTGACGCAGT	GGTCACAGGA	CGATTTCACT											1989
GACACTGCGA	ACTCTCAGGA	CTACCGGTTA	CCAAGAGGTT	AGGTGAAGTG	GTTAAACCA											2049
AACGGAACTC	TTCATCTTAA	ACTACACGTT	GAAAATCAAC	CCAATAATTC	TGTATTAAC											2109
GAATTCTGAA	CTTTTCAGGA	GGTACTGTGA	GGAAGAGCAG	GCACCAGCAG	CAGAATGGGG											2169
AATGGAGAGG	TGGGCAGGGG	TTCCAGCTTC	CCTTTGATTT	TTTGCTGCAG	ACTCATCCTT											2229
TTTAAATGAG	ACTTGTTC	CCCTCTCTT	GAGTCAGTC	AAATATGTAG	ATTGCCTTG											2289
GCAATTCTTC	TTCTCAAGCA	CTGACACTCA	TTACCGTCTG	TGATTGCCAT	TTCTTCCCAA											2349
GGCCAGTCTG	AACCTGAGGT	TGCTTTATCC	TAAAAGTTT	AACCTCAGGT	TCCAAATTCA											2409
GTAAATTTG	GAAACAGTAC	AGCTATTCT	CATCAATTCT	CTATCATGTT	GAAGTCAAAT											2469
TTGGATTTTC	CACCAAATTC	TGAATTGTA	GACATACTTG	TACGCTCACT	TGCCCCCCAGA											2529
TGCCTCCTCT	GTCCTCATTC	TTCTCTCCCA	CACAAGCAGT	CTTTTCTAC	AGCCAGTAAG											2589
GCAGCTCTGT	CRTGGTAGCA	GATGGTCCCA	TTATTCTAGG	GTCTTACTCT	TTGTATGATG											2649
AAAAGAATGT	GTTATGAATC	GGTGCTGTCA	GCCCTGCTGT	CAGACCTTCT	TCCACAGCAA											2709
ATGAGATGTA	TGCCCAAAGC	GGTAGAATTA	AAGAAGAGTA	AAATGGCTGT	TGAAGC											2765

(2) INFORMATION FOR SEQ ID NO: 28:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 467 amino acids
(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 28:

Met Thr Glu Leu Pro Ala Pro Leu Ser Tyr Phe Gln Asn Ala Gln Met
1 5 10 15

Ser Glu Asp Asn His Leu Ser Asn Thr Val Arg Ser Gln Asn Asp Asn
20 25 30

Arg Glu Arg Gln Glu His Asn Asp Arg Arg Ser Leu Gly His Pro Glu
35 40 45

Pro Leu Ser Asn Gly Arg Pro Gln Gly Asn Ser Arg Gln Val Val Glu
50 55 60

Gln Asp Glu Glu Glu Asp Glu Glu Leu Thr Leu Lys Tyr Gly Ala Lys
65 70 75 80

His Val Ile Met Leu Phe Val Pro Val Thr Leu Cys Met Val Val Val
85 90 95

Val Ala Thr Ile Lys Ser Val Ser Phe Tyr Thr Arg Lys Asp Gly Gln
100 105 110

Leu Ile Tyr Thr Pro Phe Thr Glu Asp Thr Glu Thr Val Gly Gln Arg
115 120 125

Ala Leu His Ser Ile Leu Asn Ala Ala Ile Met Ile Ser Val Ile Val
130 135 140

Val Met Thr Ile Leu Leu Val Val Leu Tyr Lys Tyr Arg Cys Tyr Lys
145 150 155 160

Val Ile His Ala Trp Leu Ile Ser Ser Leu Leu Leu Phe Phe
165 170 175

Phe Ser Phe Ile Tyr Leu Gly Glu Val Phe Lys Thr Tyr Asn Val Ala
180 185 190

Val Asp Tyr Ile Thr Val Ala Leu Leu Ile Trp Asn Phe Gly Val Val
195 200 205

Gly Met Ile Ser Ile His Trp Lys Gly Pro Leu Arg Leu Gln Gln Ala
210 215 220

Tyr Leu Ile Met Ile Ser Ala Leu Met Ala Leu Val Phe Ile Lys Tyr
225 230 235 240

Leu Pro Glu Trp Thr Ala Trp Leu Ile Leu Ala Val Ile Ser Val Tyr
245 250 255

Asp Leu Val Ala Val Leu Arg Pro Lys Gly Pro Leu Arg Met Leu Val
260 265 270

Glu Thr Ala Gln Glu Arg Asn Glu Thr Leu Phe Pro Ala Leu Ile Tyr
275 280 285

Ser Ser Thr Met Val Trp Leu Val Asn Met Ala Glu Gly Asp Pro Glu
290 295 300

Ala Gln Arg Arg Val Ser Lys Asn Ser Lys His Asn Ala Glu Ser Thr
305 310 315 320

Glu Arg Glu Ser Gln Asp Thr Val Ala Glu Asn Asp Asp Gly Gly Phe
325 330 335

Ser Glu Glu Trp Glu Ala Gln Arg Asp Ser His Leu Gly Pro His Arg
340 345 350

Ser Thr Pro Glu Ser Arg Ala Ala Val Gln Glu Leu Ser Ser Ser Ile
355 360 365

Leu Ala Gly Glu Asp Pro Glu Glu Arg Gly Val Lys Leu Gly Leu Gly
370 375 380

Asp Phe Ile Phe Tyr Ser Val Leu Val Gly Lys Ala Ser Ala Thr Ala
385 390 395 400

Ser Gly Asp Trp Asn Thr Thr Ile Ala Cys Phe Val Ala Ile Leu Ile
405 410 415

Gly Leu Cys Leu Thr Leu Leu Leu Ala Ile Phe Lys Lys Ala Leu
420 425 430

Pro Ala Leu Pro Ile Ser Ile Thr Phe Gly Leu Val Phe Tyr Phe Ala
435 440 445

Thr Asp Tyr Leu Val Gln Pro Phe Met Asp Gln Leu Ala Phe His Gln
450 455 460

Phe Tyr Ile
465

(2) INFORMATION FOR SEQ ID NO: 29:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 2765 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

- (ix) FEATURE:
- (A) NAME/KEY: CDS
 - (B) LOCATION: 249..1649

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 29:

TGGGACAGGC AGCTCCGGGG TCCGCGGTTT CACATCGGAA ACAAAACAGC GGCTGGTCTG	60
GAAGGAAACCT GAGCTACGAG CCGCGGCCGC AGCGGGCGG CGGGGAAGCG TATACTAAT	120
CTGGGAGCCT GCAAGTGACA ACAGCCTTG CGGTCTTAG ACAGCTTGGC CTGGAGGAGA	180
ACACATGAAA GAAAGAACCT CAAGAGGCTT TGTTTCTGT GAAACAGTAT TTCTATACAG	240
TTGCTCCA ATG ACA GAG TTA CCT GCA CCG TTG TCC TAC TTC CAG AAT GCA Met Thr Glu Leu Pro Ala Pro Leu Ser Tyr Phe Gln Asn Ala	290

1	5	10	
CAG ATG TCT GAG GAC AAC CAC CTG AGC AAT ACT GTA CGT AGC CAG AAT Gln Met Ser Glu Asp Asn His Leu Ser Asn Thr Val Arg Ser Gln Asn	15 20	25 30	338
GAC AAT AGA GAA CGG CAG GAG CAC AAC GAC AGA CGG AGC CTT GGC CAC Asp Asn Arg Glu Arg Gln Glu His Asn Asp Arg Arg Ser Leu Gly His	35 40	45	386
CCT GAG CCA TTA TCT AAT GGA CGA CCC CAG GGT AAC TCC CGG CAG GTG Pro Glu Pro Leu Ser Asn Gly Arg Pro Gln Gly Asn Ser Arg Gln Val	50 55	60	434
GTG GAG CAA GAT GAG GAA GAT GAG GAG CTG ACA TTG AAA TAT GGC Val Glu Gln Asp Glu Glu Asp Glu Glu Leu Thr Leu Lys Tyr Gly	65 70	75	482
GCC AAG CAT GTG ATC ATG CTC TTT GTC CCT GTG ACT CTC TGC ATG GTG Ala Lys His Val Ile Met Leu Phe Val Pro Val Thr Leu Cys Met Val	80 85	90	530
GTG GTC GTG GCT ACC ATT AAG TCA GTC AGC TTT TAT ACC CGG AAG GAT Val Val Val Ala Thr Ile Lys Ser Val Ser Phe Tyr Thr Arg Lys Asp	95 100	105	578
GGG CAG CTA ATC TAT ACC CCA TTC ACA GAA GAT ACC GAG ACT GTG GGC Gly Gln Leu Ile Tyr Thr Pro Phe Thr Glu Asp Thr Glu Thr Val Gly	115 120	125	626
CAG AGA GCC CTG CAC TCA ATT CTG AAT GCT GCC ATC ATG ATC AGT GTC Gln Arg Ala Leu His Ser Ile Leu Asn Ala Ala Ile Met Ile Ser Val	130 135	140	674
ATT GTT GTC ATG ACT ATC CTC CTG GTG GTT CTG TAT AAA TAC AGG TGC Ile Val Val Met Thr Ile Leu Leu Val Val Leu Tyr Lys Tyr Arg Cys	145 150	155	722
TAT AAG GTC ATC CAT GCC TGG CTT ATT ATA TCA TCT CTA TTG TTG CTG Tyr Lys Val Ile His Ala Trp Leu Ile Ser Ser Leu Leu Leu Leu	160 165	170	770
TTC TTT TTT TCA TTC ATT TAC TTG GGG GAA GTG TTT AAA ACC TAT AAC Phe Phe Ser Phe Ile Tyr Leu Gly Glu Val Phe Lys Thr Tyr Asn	175 180	185	818
GTT GCT GTG GAC TAC ATT ACT GTT GCA CTC CTG ATC TGG AAT TTT GGT Val Ala Val Asp Tyr Ile Thr Val Ala Leu Leu Ile Trp Asn Phe Gly	195 200	205	866
GTG GTG GGA ATG ATT TCC ATT CAC TGG AAA GGT CCA CTT CGA CTC CAG Val Val Gly Met Ile Ser Ile His Trp Lys Gly Pro Leu Arg Leu Gln	210 215	220	914
CAG GCA TAT CTC ATT ATG ATT AGT GCC CTC ATG GCC CTG GTG TTT ATC Gln Ala Tyr Leu Ile Met Ile Ser Ala Leu Met Ala Leu Val Phe Ile	225 230	235	962
AAG TAC CTC CCT GAA TGG ACT GCG TGG CTC ATC TTG GCT GTG ATT TCA Lys Tyr Leu Pro Glu Trp Thr Ala Trp Leu Ile Leu Ala Val Ile Ser	240 245	250	1010

GTA TAT GAT TTA GTG GCT GTT TTG TGT CTG AAA GGT CCA CTT CGT ATG Val Tyr Asp Leu Val Ala Val Leu Cys Leu Lys Gly Pro Leu Arg Met 255 260 265 270	1058
CTG GTT GAA ACA GCT CAG GAG AGA AAT GAA ACG CTT TTT CCA GCT CTC Leu Val Glu Thr Ala Gln Glu Arg Asn Glu Thr Leu Phe Pro Ala Leu 275 280 285	1106
ATT TAC TCC TCA ACA ATG GTG TGG TTG GTG AAT ATG GCA GAA GGA GAC Ile Tyr Ser Ser Thr Met Val Trp Leu Val Asn Met Ala Glu Gly Asp 290 295 300	1154
CCG GAA GCT CAA AGG AGA GTA TCC AAA AAT TCC AAG CAT AAT GCA GAA Pro Glu Ala Gln Arg Arg Val Ser Lys Asn Ser Lys His Asn Ala Glu 305 310 315	1202
AGC ACA GAA AGG GAG TCA CAA GAC ACT GTT GCA GAG AAT GAT GAT GGC Ser Thr Glu Arg Glu Ser Gln Asp Thr Val Ala Glu Asn Asp Asp Gly 320 325 330	1250
GGG TTC AGT GAG GAA TGG GAA GCC CAG AGG GAC AGT CAT CTA GGG CCT Gly Phe Ser Glu Glu Trp Glu Ala Gln Arg Asp Ser His Leu Gly Pro 335 340 345 350	1298
CAT CGC TCT ACA CCT GAG TCA CGA GCT GTC CAG GAA CTT TCC AGC His Arg Ser Thr Pro Glu Ser Arg Ala Ala Val Gln Glu Leu Ser Ser 355 360 365	1346
AGT ATC CTC GCT GGT GAA GAC CCA GAG GAA AGG GGA GTA AAA CTT GGA Ser Ile Leu Ala Gly Glu Asp Pro Glu Glu Arg Gly Val Lys Leu Gly 370 375 380	1394
TTG GGA GAT TTC ATT TTC TAC AGT GTT CTG GTT GGT AAA GCC TCA GCA Leu Gly Asp Phe Ile Phe Tyr Ser Val Leu Val Gly Lys Ala Ser Ala 385 390 395	1442
ACA GCC AGT GGA GAC TGG AAC ACA ACC ATA GCC TGT TTC GTA GCC ATA Thr Ala Ser Gly Asp Trp Asn Thr Ile Ala Cys Phe Val Ala Ile 400 405 410	1490
TTA ATT GGT TTG TGC CTT ACA TTA CTC CTT GCC ATT TTC AAG AAA Leu Ile Gly Leu Cys Leu Thr Leu Leu Leu Ala Ile Phe Lys Lys 415 420 425 430	1538
GCA TTG CCA GCT CTT CCA ATC TCC ATC ACC TTT GGG CTT GTT TTC TAC Ala Leu Pro Ala Leu Pro Ile Ser Ile Thr Phe Gly Leu Val Phe Tyr 435 440 445	1586
TTT GCC ACA GAT TAT CTT GTA CAG CCT TTT ATG GAC CAA TTA GCA TTC Phe Ala Thr Asp Tyr Leu Val Gln Pro Phe Met Asp Gln Leu Ala Phe 450 455 460	1634
CAT CAA TTT TAT ATC TAGCATATT GCGGTTAGAA TCCCATGGAT GTTTCTTCTT His Gln Phe Tyr Ile 465	1689
TGACTATAAC CAAATCTGGG GAGGACAAAG GTGATTTCC TGTGTCCACA TCTAACAAAG	1749
TCAAGATTC CGGCTGGACT TTTGCAGCTT CCTTCCAAGT CTTCCTGACC ACCTTGCACT	1809
ATTGGACTTT GGAAGGAGGT GCCTATAGAA AACGATTTG AACATACTTC ATCGCAGTGG	1869

ACTGTGTCCC TCGGTGCAGA AACTACCAGA TTTGAGGGAC GAGGTCAAGG AGATATGATA	1929
GGCCCGGAAG TTGCTGTGCC CCATCAGCAG CTTGACGCGT GGTCACAGGA CGATTCACT	1989
GACACTGCGA ACTCTCAGGA CTACCGGTTA CCAAGAGGTT AGGTGAAGTG GTTTAACCA	2049
AACGGAACTC TTCATCTTAA ACTACACGTT GAAAATCAAC CCAATAATTC TGTATTAAC	2109
GAATTCTGAA CTTTCAGGA GGTACTGTGA GGAAGAGCAG GCACCAGCAG CAGAATGGGG	2169
AATGGAGAGG TGGGCAGGGG TTCCAGCTTC CCTTGATTT TTTGCTGCAG ACTCATCCTT	2229
TTTAAATGAG ACTTGTTC CCCTCTCTT GAGTCAGTC AAATATGTAG ATTGCCTTG	2289
GCAATTCTTC TTCTCAAGCA CTGACACTCA TTACCGTCTG TGATTGCCAT TTCTCCAA	2349
GGCCAGTCTG AACCTGAGGT TGCTTATCC TAAAAGTTT AACCTCAGGT TCCAAATTCA	2409
GTAAATTTG GAAACAGTAC AGCTATTCT CATCAATTCT CTATCATGTT GAAGTCAAAT	2469
TG GGATTTTC CACCAAATTC TGAATTGTA GACATACTTG TACGCTCACT TGCCCCCAGA	2529
TGCCTCCTCT GTCCTCATTC TTCTCTCCA CACAAGCAGT CTTTTCTAC AGCCAGTAAG	2589
GCAGCTCTGT CRTGGTAGCA GATGGTCCA TTATTCTAGG GTCTTACTCT TTGTATGATG	2649
AAAAGAATGT GTTATGAATC GGTGCTGTCA GCCCTGCTGT CAGACCTTCT TCCACAGCAA	2709
ATGAGATGTA TGCCCAAAGC GGTAGAATTA AAGAAGAGTA AAATGGCTGT TGAAGC	2765

(2) INFORMATION FOR SEQ ID NO: 30:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 467 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 30:

Met Thr Glu Leu Pro Ala Pro Leu Ser Tyr Phe Gln Asn Ala Gln Met	
1 5 10 15	
Ser Glu Asp Asn His Leu Ser Asn Thr Val Arg Ser Gln Asn Asp Asn	
20 25 30	
Arg Glu Arg Gln Glu His Asn Asp Arg Arg Ser Leu Gly His Pro Glu	
35 40 45	
Pro Leu Ser Asn Gly Arg Pro Gln Gly Asn Ser Arg Gln Val Val Glu	
50 55 60	
Gln Asp Glu Glu Glu Asp Glu Glu Leu Thr Leu Lys Tyr Gly Ala Lys	
65 70 75 80	
His Val Ile Met Leu Phe Val Pro Val Thr Leu Cys Met Val Val Val	
85 90 95	
Val Ala Thr Ile Lys Ser Val Ser Phe Tyr Thr Arg Lys Asp Gly Gln	
100 105 110	

Leu Ile Tyr Thr Pro Phe Thr Glu Asp Thr Glu Thr Val Gly Gln Arg
115 120 125

Ala Leu His Ser Ile Leu Asn Ala Ala Ile Met Ile Ser Val Ile Val
130 135 140

Val Met Thr Ile Leu Leu Val Val Leu Tyr Lys Tyr Arg Cys Tyr Lys
145 150 155 160

Val Ile His Ala Trp Leu Ile Ser Ser Leu Leu Leu Leu Phe Phe
165 170 175

Phe Ser Phe Ile Tyr Leu Gly Glu Val Phe Lys Thr Tyr Asn Val Ala
180 185 190

Val Asp Tyr Ile Thr Val Ala Leu Leu Ile Trp Asn Phe Gly Val Val
195 200 205

Gly Met Ile Ser Ile His Trp Lys Gly Pro Leu Arg Leu Gln Gln Ala
210 215 220

Tyr Leu Ile Met Ile Ser Ala Leu Met Ala Leu Val Phe Ile Lys Tyr
225 230 235 240

Leu Pro Glu Trp Thr Ala Trp Leu Ile Leu Ala Val Ile Ser Val Tyr
245 250 255

Asp Leu Val Ala Val Leu Cys Leu Lys Gly Pro Leu Arg Met Leu Val
260 265 270

Glu Thr Ala Gln Glu Arg Asn Glu Thr Leu Phe Pro Ala Leu Ile Tyr
275 280 285

Ser Ser Thr Met Val Trp Leu Val Asn Met Ala Glu Gly Asp Pro Glu
290 295 300

Ala Gln Arg Arg Val Ser Lys Asn Ser Lys His Asn Ala Glu Ser Thr
305 310 315 320

Glu Arg Glu Ser Gln Asp Thr Val Ala Glu Asn Asp Asp Gly Gly Phe
325 330 335

Ser Glu Glu Trp Glu Ala Gln Arg Asp Ser His Leu Gly Pro His Arg
340 345 350

Ser Thr Pro Glu Ser Arg Ala Ala Val Gln Glu Leu Ser Ser Ser Ile
355 360 365

Leu Ala Gly Glu Asp Pro Glu Glu Arg Gly Val Lys Leu Gly Leu Gly
370 375 380

Asp Phe Ile Phe Tyr Ser Val Leu Val Gly Lys Ala Ser Ala Thr Ala
385 390 395 400

Ser Gly Asp Trp Asn Thr Thr Ile Ala Cys Phe Val Ala Ile Leu Ile
405 410 415

Gly Leu Cys Leu Thr Leu Leu Leu Ala Ile Phe Lys Lys Ala Leu
420 425 430

Pro Ala Leu Pro Ile Ser Ile Thr Phe Gly Leu Val Phe Tyr Phe Ala
435 440 445

Thr Asp Tyr Leu Val Gln Pro Phe Met Asp Gln Leu Ala Phe His Gln
450 455 460

Phe Tyr Ile
465

(2) INFORMATION FOR SEQ ID NO: 31:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2765 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 249..1649

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 31:

TGGGACAGGC AGCTCCGGGG TCCGCGGTTT CACATCGGAA ACAAAACAGC GGCTGGTCTG	60
GAAGGAAACCT GAGCTACGAG CCGCGGCCGG AGCGGGCGG CGGGGAAGCG TATACTTAAT	120
CTGGGAGCCT GCAAGTGACA ACAGCCTTTG CGGTCTTAG ACAGCTTGGC CTGGAGGAGA	180
ACACATGAAA GAAAGAACCT CAAGAGGCTT TGTTTCTGT GAAACAGTAT TTCTATACAG	240
TTGCTCCA ATG ACA GAG TTA CCT GCA CCG TTG TCC TAC TTC CAG AAT GCA	290
Met Thr Glu Leu Pro Ala Pro Leu Ser Tyr Phe Gln Asn Ala	
1 5 10	
CAG ATG TCT GAG GAC AAC CAC CTG AGC AAT ACT GTA CGT AGC CAG AAT	338
Gln Met Ser Glu Asp Asn His Leu Ser Asn Thr Val Arg Ser Gln Asn	
15 20 25 30	
GAC AAT AGA GAA CGG CAG GAG CAC AAC GAC AGA CGG AGC CTT GGC CAC	386
Asp Asn Arg Glu Arg Gln Glu His Asn Asp Arg Arg Ser Leu Gly His	
35 40 45	
CCT GAG CCA TTA TCT AAT GGA CGA CCC CAG GGT AAC TCC CGG CAG GTG	434
Pro Glu Pro Leu Ser Asn Gly Arg Pro Gln Gly Asn Ser Arg Gln Val	
50 55 60	
GTG GAG CAA GAT GAG GAA GAT GAG GAG CTG ACA TTG AAA TAT GGC	482
Val Glu Gln Asp Glu Glu Asp Glu Glu Leu Thr Leu Lys Tyr Gly	
65 70 75	
GCC AAG CAT GTG ATC ATG CTC TTT GTC CCT GTG ACT CTC TGC ATG GTG	530
Ala Lys His Val Ile Met Leu Phe Val Pro Val Thr Leu Cys Met Val	
80 85 90	
GTG GTC GTG GCT ACC ATT AAG TCA GTC AGC TTT TAT ACC CGG AAG GAT	578
Val Val Val Ala Thr Ile Lys Ser Val Ser Phe Tyr Thr Arg Lys Asp	
95 100 105 110	
GGG CAG CTA ATC TAT ACC CCA TTC ACA GAA GAT ACC GAG ACT GTG GGC	626

Gly Gln Leu Ile Tyr Thr Pro Phe Thr Glu Asp Thr Glu Thr Val Gly	115	120	125	
CAG AGA GCC CTG CAC TCA ATT CTG AAT GCT GCC ATC ATG ATC AGT GTC				674
Gln Arg Ala Leu His Ser Ile Leu Asn Ala Ala Ile Met Ile Ser Val	130	135	140	
ATT GTT GTC ATG ACT ATC CTC CTG GTG GTT CTG TAT AAA TAC AGG TGC				722
Ile Val Val Met Thr Ile Leu Leu Val Val Leu Tyr Lys Tyr Arg Cys	145	150	155	
TAT AAG GTC ATC CAT GCC TGG CTT ATT ATA TCA TCT CTA TTG TTG CTG				770
Tyr Lys Val Ile His Ala Trp Leu Ile Ser Ser Leu Leu Leu Leu	160	165	170	
TTC TTT TCA TTC ATT TAC TTG GGG GAA GTG TTT AAA ACC TAT AAC				818
Phe Phe Phe Ser Phe Ile Tyr Leu Gly Glu Val Phe Lys Thr Tyr Asn	175	180	185	
GTT GCT GTG GAC TAC ATT ACT GTT GCA CTC CTG ATC TGG AAT TTT GGT				866
Val Ala Val Asp Tyr Ile Thr Val Ala Leu Leu Ile Trp Asn Phe Gly	195	200	205	
GTG GTG GGA ATG ATT TCC ATT CAC TGG AAA GGT CCA CTT CGA CTC CAG				914
Val Val Gly Met Ile Ser Ile His Trp Lys Gly Pro Leu Arg Leu Gln	210	215	220	
CAG GCA TAT CTC ATT ATG ATT AGT GCC CTC ATG GCC CTG GTG TTT ATC				962
Gln Ala Tyr Leu Ile Met Ile Ser Ala Leu Met Ala Leu Val Phe Ile	225	230	235	
AAG TAC CTC CCT GAA TGG ACT GCG TGG CTC ATC TTG GCT GTG ATT TCA				1010
Lys Tyr Leu Pro Glu Trp Thr Ala Trp Leu Ile Leu Ala Val Ile Ser	240	245	250	
GTA TAT GAT TTA GTG GCT GTT TTG TGT CCG AAA GGT CCA CTT CAT ATG				1058
Val Tyr Asp Leu Val Ala Val Leu Cys Pro Lys Gly Pro Leu His Met	255	260	265	
CTG GTT GAA ACA GCT CAG GAG AGA AAT GAA ACG CTT TTT CCA GCT CTC				1106
Leu Val Glu Thr Ala Gln Glu Arg Asn Glu Thr Leu Phe Pro Ala Leu	275	280	285	
ATT TAC TCC TCA ACA ATG GTG TGG TTG GTG AAT ATG GCA GAA GGA GAC				1154
Ile Tyr Ser Ser Thr Met Val Trp Leu Val Asn Met Ala Glu Gly Asp	290	295	300	
CCG GAA GCT CAA AGG AGA GTA TCC AAA AAT TCC AAG CAT AAT GCA GAA				1202
Pro Glu Ala Gln Arg Arg Val Ser Lys Asn Ser Lys His Asn Ala Glu	305	310	315	
AGC ACA GAA AGG GAG TCA CAA GAC ACT GTT GCA GAG AAT GAT GAT GGC				1250
Ser Thr Glu Arg Glu Ser Gln Asp Thr Val Ala Glu Asn Asp Asp Gly	320	325	330	
GGG TTC AGT GAG GAA TGG GAA GCC CAG AGG GAC AGT CAT CTA GGG CCT				1298
Gly Phe Ser Glu Glu Trp Glu Ala Gln Arg Asp Ser His Leu Gly Pro	335	340	345	
CAT CGC TCT ACA CCT GAG TCA CGA GCT GCT GTC CAG GAA CTT TCC AGC				1346
His Arg Ser Thr Pro Glu Ser Arg Ala Ala Val Gln Glu Leu Ser Ser	355	360	365	

AGT ATC CTC GCT GGT GAA GAC CCA GAG GAA AGG GGA GTA AAA CTT GGA Ser Ile Leu Ala Gly Glu Asp Pro Glu Glu Arg Gly Val Lys Leu Gly 370 375 380	1394
TTG GGA GAT TTC ATT TTC TAC AGT GTT CTG GTT GGT AAA GCC TCA GCA Leu Gly Asp Phe Ile Phe Tyr Ser Val Leu Val Gly Lys Ala Ser Ala 385 390 395	1442
ACA GCC AGT GGA GAC TGG AAC ACA ACC ATA GCC TGT TTC GTA GCC ATA Thr Ala Ser Gly Asp Trp Asn Thr Thr Ile Ala Cys Phe Val Ala Ile 400 405 410	1490
TTA ATT GGT TTG TGC CTT ACA TTA TTA CTC CTT GCC ATT TTC AAG AAA Leu Ile Gly Leu Cys Leu Thr Leu Leu Leu Ala Ile Phe Lys Lys 415 420 425 430	1538
GCA TTG CCA GCT CTT CCA ATC TCC ATC ACC TTT GGG CTT GTT TTC TAC Ala Leu Pro Ala Leu Pro Ile Ser Ile Thr Phe Gly Leu Val Phe Tyr 435 440 445	1586
TTT GCC ACA GAT TAT CTT GTA CAG CCT TTT ATG GAC CAA TTA GCA TTC Phe Ala Thr Asp Tyr Leu Val Gln Pro Phe Met Asp Gln Leu Ala Phe 450 455 460	1634
CAT CAA TTT TAT ATC TAGCATATTG GCGGTTAGAA TCCCATGGAT GTTTCTTCTT His Gln Phe Tyr Ile 465	1689
TGACTATAAC CAAATCTGGG GAGGACAAAG GTGATTTCC TGTGTCCACA TCTAACAAAG TCAAGATTCC CGGCTGGACT TTTGCAGCTT CCTTCCAAGT CTTCCTGACC ACCTTGCAC ATTGGACTTT GGAAGGAGGT GCCTATAGAA AACGATTTG AACATACTTC ATCGCAGTGG ACTGTGTCCC TCGGTGCAGA AACTACCAGA TTTGAGGGAC GAGGTCAAGG AGATATGATA GGCCCCGAAG TTGCTGTGCC CCATCAGCAG CTTGACGCGT GGTCACAGGA CGATTTCACT GACACTGCGA ACTCTCAGGA CTACCGTTA CCAAGAGGTT AGGTGAAGTG GTTAAACCA AACGGAACTC TTCATCTTAA ACTACACGTT GAAAATCAAC CCAATAATTC TGTATTAAC GAATTCTGAA CTTTTCAGGA GGTACTGTGA GGAAGAGCAG GCACCAGCAG CAGAATGGGG AATGGAGAGG TGGGCAGGGG TTCCAGCTTC CCTTGATTT TTTGCTGCAG ACTCATCCTT TTTAAATGAG ACTTGTTC CCCTCTCTT GAGTCAAGTC AAATATGTAG ATTGCCTTG GCAATTCTTC TTCTCAAGCA CTGACACTCA TTACCGTCTG TGATTGCCAT TTCTTCCCAA GGCCAGTCTG AACCTGAGGT TGCTTATCC TAAAAGTTT AACCTCAGGT TCCAAATTCA GTAAATTTG GAAACAGTAC AGCTATTCT CATCAATTCT CTATCATGTT GAAGTCAAAT TTGGATTTTC CACCAAATTC TGAATTGTA GACATACTTG TACGCTCACT TGCCCCCAGA TGCCTCCTCT GTCCTCATTC TTCTCTCCCA CACAAGCAGT CTTTTCTAC AGCCAGTAAG GCAGCTCTGT CRTGGTAGCA GATGGTCCCA TTATTCTAGG GTCTTACTCT TTGTATGATG AAAAGAATGT GTTATGAATC GGTGCTGTCA GCCCTGCTGT CAGACCTTCT TCCACAGCAA	1749 1809 1869 1929 1989 2049 2109 2169 2229 2289 2349 2409 2469 2529 2589 2649 2709

ATGAGATGTA TGCCCAAAGC GGTAGAATTAAAGAAGAGTA AAATGGCTGT TGAAGC

2765

(2) INFORMATION FOR SEQ ID NO: 32:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 467 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 32:

Met Thr Glu Leu Pro Ala Pro Leu Ser Tyr Phe Gln Asn Ala Gln Met
1 5 10 15

Ser Glu Asp Asn His Leu Ser Asn Thr Val Arg Ser Gln Asn Asp Asn
20 25 30

Arg Glu Arg Gln Glu His Asn Asp Arg Arg Ser Leu Gly His Pro Glu
35 40 45

Pro Leu Ser Asn Gly Arg Pro Gln Gly Asn Ser Arg Gln Val Val Glu
50 55 60

Gln Asp Glu Glu Glu Asp Glu Glu Leu Thr Leu Lys Tyr Gly Ala Lys
65 70 75 80

His Val Ile Met Leu Phe Val Pro Val Thr Leu Cys Met Val Val Val
85 90 95

Val Ala Thr Ile Lys Ser Val Ser Phe Tyr Thr Arg Lys Asp Gly Gln
100 105 110

Leu Ile Tyr Thr Pro Phe Thr Glu Asp Thr Glu Thr Val Gly Gln Arg
115 120 125

Ala Leu His Ser Ile Leu Asn Ala Ala Ile Met Ile Ser Val Ile Val
130 135 140

Val Met Thr Ile Leu Leu Val Val Leu Tyr Lys Tyr Arg Cys Tyr Lys
145 150 155 160

Val Ile His Ala Trp Leu Ile Ser Ser Leu Leu Leu Leu Phe Phe
165 170 175

Phe Ser Phe Ile Tyr Leu Gly Glu Val Phe Lys Thr Tyr Asn Val Ala
180 185 190

Val Asp Tyr Ile Thr Val Ala Leu Leu Ile Trp Asn Phe Gly Val Val
195 200 205

Gly Met Ile Ser Ile His Trp Lys Gly Pro Leu Arg Leu Gln Gln Ala
210 215 220

Tyr Leu Ile Met Ile Ser Ala Leu Met Ala Leu Val Phe Ile Lys Tyr
225 230 235 240

Leu Pro Glu Trp Thr Ala Trp Leu Ile Leu Ala Val Ile Ser Val Tyr
245 250 255

Asp Leu Val Ala Val Leu Cys Pro Lys Gly Pro Leu His Met Leu Val

260	265	270
Glu Thr Ala Gln Glu Arg Asn Glu	Thr Leu Phe Pro Ala	Leu Ile Tyr
275	280	285
Ser Ser Thr Met Val Trp Leu Val Asn Met Ala	Glu Gly Asp Pro	Glu
290	295	300
Ala Gln Arg Arg Val Ser Lys Asn Ser Lys His	Asn Ala Glu Ser	Thr
305	310	315
Glu Arg Glu Ser Gln Asp Thr Val Ala Glu Asn Asp	Asp Gly Gly	Phe
325	330	335
Ser Glu Glu Trp Glu Ala Gln Arg Asp Ser His	Leu Gly Pro	His Arg
340	345	350
Ser Thr Pro Glu Ser Arg Ala Ala Val Gln Glu	Leu Ser Ser	Ile
355	360	365
Leu Ala Gly Glu Asp Pro Glu Glu Arg Gly Val	Lys Leu Gly Leu	Gly
370	375	380
Asp Phe Ile Phe Tyr Ser Val Leu Val Gly Lys	Ala Ser Ala Thr	Ala
385	390	395
Ser Gly Asp Trp Asn Thr Thr Ile Ala Cys	Phe Val Ala Ile	Ile
405	410	415
Gly Leu Cys Leu Thr Leu Leu Leu Ala Ile Phe	Lys Lys Ala Leu	
420	425	430
Pro Ala Leu Pro Ile Ser Ile Thr Phe Gly	Leu Val Phe	Tyr Phe Ala
435	440	445
Thr Asp Tyr Leu Val Gln Pro Phe Met Asp Gln	Leu Ala Phe	His Gln
450	455	460
Phe Tyr Ile		
465		